We Claim:

1. A method for detecting the presence of a post-translational modification on a target protein within a sample, comprising:
   (1) computationally analyzing amino acid sequence of said target protein to identify one or more candidate site for said post-translational modification;
   (2) computationally identifying the amino acid sequence of one or more fragment of said target protein, said fragment predictably results from a treatment of said target protein within said sample, and said fragment encompasses said potential post-translational modification site and a PET (proteome epitope tag) unique to said fragment within said sample;
   (3) generating a capture agent that specifically binds said PET, and immobilizing said capture agent to a support;
   (4) subjecting said sample to said treatment to render said fragment soluble in solution, and contacting said sample after said treatment to said capture agent;
   (5) detecting, on said fragment bound to said capture agent, the presence or absence of said post-translational modification.

2. The method of claim 1, wherein said post-translational modification is acetylation, amidation, deamidation, prenylation, formylation, glycosylation, hydroxylation, methylation, myristoylation, phosphorylation, ubiquitination, ribosylation or sulphation.

3. The method of claim 2, wherein said post-translational modification is phosphorylation on tyrosine, serine or threonine.

4. The method of claim 1, wherein said step of computationally analyzing amino acid sequences includes a Nearest-Neighbor Analysis that identifies said PET based on criteria that also include one or more of pI, charge, steric, solubility, hydrophobicity, polarity and solvent exposed area.

5. The method of claim 4, further comprising determining the specificity of said capture agent generated in (3) against one or more nearest neighbor(s), if any, of said PET.

6. The method of claim 5, wherein peptide competition assay is used in determining the specificity of said capture agent generated in (3) against said nearest neighbor(s) of said PET.

7. The method of claim 1, wherein said step of computationally analyzing amino acid sequences includes a solubility analysis that identifies said PET that are predicted to have at least a threshold solubility under a designated solution condition.

8. The method of claim 1, wherein the length of said PET is selected from 5-10 amino acids, 10-15 amino acids, 15-20 amino acids, 20-25 amino acids, 25-30 amino acids, or 30-40 amino acids.

9. The method of claim 1, wherein said capture agent is a full-length antibody, or a functional antibody fragment selected from: an Fab fragment, an $F(ab')_2$ fragment, an Fd fragment, an Fv fragment, a dAb fragment, an isolated complementarity determining region (CDR), a single chain antibody (scFv), or derivative thereof.

10. The method of claim 1, wherein said capture agent is nucleotides; nucleic acids; PNA (peptide nucleic acids); proteins; peptides; carbohydrates; artificial polymers; or small organic molecules.

11. The method of claim 1, wherein said capture agent is aptamers, scaffolded peptides, or small organic molecules.

12. The method of claim 1, wherein said treatment is denaturation and/or fragmentation of said sample by a protease, a chemical agent, physical shearing, or sonication.

13. The method of claim 12, wherein said denaturation is thermo-denaturation or chemical denaturation.

14. The method of claim 13, wherein said thermo-denaturation is followed by or concurrent with proteolysis using thermo-stable proteases.

15. The method of claim 13, wherein said thermo-denaturation comprises two or more cycles of thermo-denaturation followed by protease digestion.

16. The method of claim 12, wherein said fragmentation is carried out by a protease selected from trypsin, chymotrypsin, pepsin, papain, carboxypeptidase, calpain, subtilisin, gluc-C, endo lys-C, or proteinase K.

17. The method of claim 1, wherein said sample is a body fluid selected from: saliva, mucous, sweat, whole blood, serum, urine, amniotic fluid, genital fluid, fecal material, marrow, plasma, spinal fluid, pericardial fluid, gastric fluid, abdominal fluid, peritoneal fluid, pleural fluid, synovial fluid, cyst fluid, cerebrospinal fluid, lung lavage fluid, lymphatic fluid, tears, prostatitc fluid, extraction from other body parts, or secretion from other glands; or from supernatant, whole cell lysate, or cell fraction obtained by lysis and fractionation of cellular material, extract or fraction of cells obtained directly from a biological entity or cells grown in an artificial environment.

18. The method of claim 1, wherein said sample is obtained from human, mouse, rat, frog (Xenopus), fish (zebra fish), fly (*Drosophila melanogaster*), nematode (*C. elegans*), fission or budding yeast, or plant (*Arabidopsis thaliana*).

19. The method of claim 1, wherein said sample is produced by treatment of membrane bound proteins.

20. The method of claim 1, wherein said treatment is carried out under conditions to preserve said post-translational modification.

21. The method of claim 1, wherein said PET and said candidate site for said post-translational modification do not overlap.

22. The method of claim 1, wherein said capture agent is optimized for selectivity for said PET under denaturing conditions.

23. The method of claim 1, wherein step (5) is effectuated by using a secondary capture agent specific for said post-translational modification, wherein said secondary capture agent is labeled by a detectable moiety selected from: an enzyme, a fluorescent label, a stainable dye, a chemilumninescent compound, a colloidal particle, a radioactive isotope, a near-infrared dye, a DNA dendrimer, a water-soluble quantum dot, a latex bead, a selenium particle, or a europium nanoparticle.

24. The method of claim 23, wherein said post-translational modification is phosphorylation, and said secondary capture agent is a labeled secondary antibody specific for phosphorylated tyrosine, phosphorylated serine, or phosphorylated threonine.

25. The method of claim 24, wherein said secondary antibody is labeled by an enzyme or a fluorescent group.

26. The method of claim 25, wherein said enzyme is HRP (horse radish peroxidase).

27. The method of claim 23, wherein said post-translational modification is phosphorylation, and said secondary capture agent is a fluorescent dye that specifically stains phosphoamino acids.

28. The method of claim 27, wherein said fluorescent dye is Pro-Q Diamond dye.

29. The method of claim 23, wherein said post-translational modification is glycosylation, and said labeled secondary capture agent is a labeled lectin specific for one or more sugar moieties attached to the glycosylation site.

30. The method of claim 23, wherein said post-translational modification is ubiquitination, and said labeled secondary capture agent is a labeled secondary antibody specific for ubiquitin.

31. The method of claim 1, wherein said sample contains billion molar excess of unrelated proteins or fragments thereof relative to said fragment.

32. The method of claim 1, further comprising qauntitating the amount of said fragment

bound to said capture agent.

33. The method of claim 1, wherein step (3) is effectuated by immunizing an animal with an antigen comprising said PET sequence.

34. The method of claim 33, wherein the N- or C-terminus, or both, of said PET sequence are blocked to eliminate free N- or C-terminus, or both.

35. The method of claim 34, wherein the N- or C-terminus of said PET sequence are blocked by fusing the PET sequence to a heterologous carrier polypeptide, or blocked by a small chemical group.

36. The method of claim 35, wherein said carrier is KLH or BSA.

37. An array of capture agents for identifying all potential substrates of a kinase within a proteome, comprising a plurality of capture agents, each immobilized on a distinct addressable location on solid support, each of said capture agents specifically binds a PET uniquely associated with a peptide fragment that predictably results from a treatment of all proteins within said proteome, wherein said peptide fragment encompasses one or more potential phosphorylation sites of said kinase.

38. The array of claim 37, wherein said solid support is beads or an array device in a manner that encodes the identity of said capture agents disposed thereon.

39. The array of claim 38, wherein said array includes 100 or more different capture agents.

40. The array of claim 38, wherein said array device includes a diffractive grating surface.

41. The array of claim 38, wherein said capture agents are antibodies or antigen binding portions thereof, and said array is an arrayed ELISA.

42. The array of claim 38, wherein said array device is a surface plasmon resonance array.

43. The array of claim 38, wherein said beads are encoded as a virtual array.

44. A method of identifying, in a sample, potential substrates of a kinase, comprising:

(1) computationally analyzing amino acid sequences of all proteins in a proteome to identify all candidate phosphorylation sites for said kinase;

(2) computationally identifying all peptide fragments encompassing one or more said candidate phosphorylation sites, said fragments predictably result from a treatment of all proteins within said proteome;

(3) for each said fragments identified in (2), identifying one PET unique to said

fragment within said sample;

(4) obtaining capture agents specific for each PET identified in (3), respectively, and immobilizing said capture agents to generate the array of claim 37;

(5) contacting said array of capture agents with a sample of said proteome subjected to said treatment, and

(6) detecting the presence of phosphorylated residues within any fragments bound to said capture agents, if any,

wherein the presence of phosphorylated residues within a specific fragment bound to a specific capture agent is indicative that the protein, from which said specific fragment is derived from, is a substrate of said kinase.

45. The method of claim 44, wherein said proteome is a human proteome.

46. The method of claim 44, wherein said candidate phosphorylation sites are predicted based on the consensus sequence of phosphorylation by said kinase.

47. The method of claim 46, wherein said consensus sequence is obtained from a phosphorylation site database.

48. The method of claim 44, wherein said sample is pre-treated by an agent that is a known agonist of said kinase, or a known agonist of the signaling pathway to which said kinase belongs.

49. The method of claim 44, wherein said treatment is carried out under conditions to preserve phosphorylation.

50. The method of claim 44, further comprising verifying phosphorylation of said identified substrate by said kinase in vitro or in vivo.

51. The method of claim 44, wherein said proteome and said kinase are from the same organism.

52. The method of claim 44, wherein step (6) is effectuated by using a labeled secondary capture agent specific for phosphorylated residues.

53. An array of capture agents for identifying all potential substrates of an enzyme catalyzing post-translational modification within a proteome, comprising a plurality of capture agents, each immobilized on a distinct addressable location on solid

support, each of said capture agents specifically binds a PET uniquely associated with a peptide fragment that predictably results from a treatment of all proteins within said proteome, wherein said peptide fragment encompasses one or more potential post-translational modification sites of said enzyme.

54. A method of identifying, in a sample, potential substrates of an enzyme that catalyze a post-translational modification selected from acetylation, amidation, deamidation, prenylation, formylation, glycosylation, hydroxylation, methylation, myristoylation, phosphorylation, ubiquitination, ribosylation or sulphation, comprising:

(1) computationally analyzing amino acid sequences of all proteins in a proteome to identify all candidate post-translational modification sites for said enzyme;

(2) computationally identifying all peptide fragments encompassing one or more said candidate post-translational modification sites, said fragments predictably result from a treatment of all proteins within said proteome;

(3) for each said fragments identified in (2), identifying one PET unique to said fragment within said sample;

(4) obtaining capture agents specific for each PET identified in (3), respectively, and immobilizing said capture agents in the array of claim 53;

(5) contacting said array of capture agents with a sample of said proteome subjected to said treatment, and

(6) detecting the presence of residues with said post-translational modification within any fragments bound to said capture agents, if any,

wherein the presence of residues with said post-translational modification within a specific fragment bound to a specific capture agent is indicative that the protein, from which said specific fragment is derived from, is a substrate of said enzyme.

55. An array of capture agents for determining which, if any, of a selected number of signal transduction pathways within a proteome is activated or inhibited in response to a stimulation, comprising:

a plurality of capture agents, each immobilized on a distinct addressable location on solid support, each of said capture agents specifically binds a unique PET associated with a peptide fragment that predictably results from a treatment of one or more key proteins of said signal transduction pathways, said peptide fragment encompasses one or more sites predictably post-translationally modified upon activation or inhibition of said pathway;

wherein each of said signal transduction pathways is represented by one or more said

key proteins.

56. The array of claim 55, wherein said signal transduction pathways are immune pathways activated by IL-4, IL-13, or Token-like receptor; seven-transmembrane receptor pathways activated by adrenergic, PAC1 receptor, *Dictyostelium discoideum* cAMP chemotaxis, Wnt/Ca^{2+}/cGMP, or G Protein-independent seven transmembrane receptor; circadian rhythm pathway of murine or *Drosophila*; insulin pathway; FAS pathway; TNF pathway; G-Protein coupled receptor pathways; integrin pathways; mitogen-activated protein kinase pathways of MAPK, JNK, or p38; estrogen receptor pathway; phosphoinositide 3-kinase pathway; Transforming Growth Factor-β (TGF-β) pathway; B Cell antigen receptor pathway; Jak-STAT pathway; STAT3 pathway; T Cell signal transduction pathway; Type 1 Interferon (α/β) pathway; jasmonate biochemical pathway; or jasmonate signaling pathway.

57. The array of claim 55, wherein said proteome is that of human, mouse, rat, frog (Xenopus), fish (zebra fish), fly (*Drosophila melanogaster*), nematode (*C. elegans*), fission or budding yeast, or plant (*Arabidopsis thaliana*).

58. The array of claim 55, wherein said post-translational modification is phosphorylation on a tyrosine, a serine, or a threonine residue.

59. The array of claim 55, wherein said stimulation is treatment of cells by a growth factor, a cytokine, a hormone, a steroid, a lipid, an antigen, a small molecule (Ca^{2+}, cAMP, cGMP), an osmotic shock, a heat or cold shock, a pH change, a change in ionic strength, a mechanical force, a viral or bacterial infection, or an attachment or detachment from a neighboring cell or a surface with or without a coated protein.

60. The array of claim 55, wherein activation or inhibition of at least one of said signal transduction pathways is manifested by a type of post-translational modification different from those of other signal transduction pathways.

61. The array of claim 55, wherein at least 3, 5, 10, 20, 50, 100, 200, 500, or 1000 signaling pathways are represented.

62. The array of claim 55, wherein signaling pathways of at least two different organisms are represented.

63. The array of claim 62, wherein similar signaling pathways of different organisms are represented.

64. The array of claim 55, wherein all capture agents are specific for proteins belonging to the same signal transduction pathway, and wherein all proteins of said signal transduction pathway that are predictably post-translationally modified are represented.

65. The array of claim 55, wherein one or more of said key proteins are post-translationally modified upon activation or inhibition of at least two of said signal transduction pathways.

66. The array of claims 37, 53 or 55, further including instructions for:

(1) denaturing and/or fragmentation of a sample containing polypeptide analytes, in a way compatible with the array;

(2) detecting interaction of said polypeptide analytes or fragments thereof with said capture agents.

67. The array of claim 66, wherein the instructions further includes one or more of: data for calibration procedures and preparation procedures, and statistical data on performance characteristics of the capture agents.

68. The array of claims 37, 53 or 55, wherein the array has a recovery rate of at least 50 percent.

69. The array of claims 37, 53 or 55, wherein the array has an overall positive predictive value for occurrence of proteins in said sample of at least 90 percent.

70. The array of claims 37, 53 or 55, wherein the array has an overall diagnostic sensitivity (DSN) for occurrence of proteins in said sample of 99 percent or higher.

71. The array of claims 37, 53 or 55, wherein said array comprises at least 1,000 or 10,000 different capture agents bound to said support.

72. The array of claims 37, 53 or 55, wherein said capture agents are bound to said support at a density of 100 capture agents /cm^2.

73. The array of claims 37, 53 or 55, further including one or more labeled reference peptides including PET portions that bind to said capture agents, wherein said binding of said capture agents with said polypeptide analytes is detected by a competitive binding assay with said reference peptides.

74. The array of claims 37, 53 or 55, wherein the addressable array is collection of beads, each of which comprises a discrete species of capture agent and one or more labels which identify the bead.

75. A method of using the array of claim 55 for determining which, if any, of a selected number of signal transduction pathways within a sample from a proteome is activated or inhibited in response to a stimulation, comprising:

(1) subjecting said sample to said stimulation;

(2) subjecting said sample to the treatment of claim 55 to render said peptide fragment of claim 55 soluble in solution;

(3) contacting said sample after said treatment to the array of claim 55;

(4) detecting the presence, and/or quantitate the amount of post-translationally modified residues within any fragments bound to said capture agents, if any,

wherein a change in the presence and/or amount of post-translationally modified residues within a specific fragment bound to a specific capture agent on said array, after said stimulation, is indicative that the signal transduction pathway represented by said specific fragment is activated or inhibited.

76. The method of claim 75, wherein said stimulation is effectuated by a candidate analog of a drug, and wherein activation or inhibition of a specific signal transduction pathway is monitored.

77. The method of claim 76, wherein said specific signal transduction pathway is one that is affected by said drug.

78. The method of claim 77, further comprising comparing the degree of activation / inhibition of said specific signal transduction pathway by said analog and said drug.

79. The method of claim 77, wherein said specific signal transduction pathway is one that mediates a side effect of said drug.

80. A business method for a biotechnology or pharmaceutical business, the method comprising:

(i) identifying, using the method of claim 44, one or more substrates for an enzyme catalyzing a post-translational modification;

(ii) optionally, verifying the post-translational modification of said substrates by said enzyme;

(iii) licensing to a third party the right to manufacture, or explore the use of said substrate as a target of said enzyme.

81. A business method for providing protein detection arrays for identifying substrates of a post-translational modification enzyme, the method comprising:

(i) identifying, within a proteome, one or more protein(s) or fragments thereof that have at least one site for said potential post-translational modification;

(ii) identifying one or more PETs for each of one or more protein(s) or fragments thereof identified in (i);

(iii) generating one or more capture agent(s) for each of said PETs identified in (ii), each of said capture agent(s) specifically bind one of said PETs for which said capture agent(s) is generated;

(iv) fabricating arrays of capture agent(s) generated in (iii), wherein each of said capture agents is bound to a different discrete region or address of said solid support;

(v) packaging said arrays of capture agent(s) in (iv) for use in diagnostic and/or research experimentation.

82. The business method of claim 81, further comprising marketing said arrays of capture agent(s).

83. The business method of claim 81, further comprising distributing said arrays of capture agent(s).

84. A composition comprising a plurality of capture agents, wherein said plurality of capture agents are, collectively, capable of specifically interacting with all potential substrates of a post-translational modification enzyme within an organism's proteome, and wherein each of said capture agents is able to recognize and interact with only one PET within said potential substrate or fragment thereof containing the post-translational modification site.

85. The composition of claim 84, wherein said capture agents are selected from the group consisting of: nucleotides; nucleic acids; PNA (peptide nucleic acids); proteins; peptides; carbohydrates; artificial polymers; and small organic molecules.

86. The composition of claim 85, wherein said capture agents are antibodies, or antigen binding fragments thereof.

87. The composition of claim 86, wherein said capture agent is a full-length antibody, or a functional antibody fragment selected from: an Fab fragment, an $F(ab')_2$ fragment, an Fd fragment, an Fv fragment, a dAb fragment, an isolated complementarity determining region (CDR), a single chain antibody (scFv), or derivative thereof.

88. The composition of claim 86, wherein each of said capture agents is a single chain antibody.

89. A business method for generating arrays of capture agents for marketing in research and development, the method comprising:

(1) identifying one or more protein(s), a post-translational modification of which protein(s) represent the activation of at least one signal transduction pathway within an organism;

(2) identifying one or more PETs for each of said protein(s), or fragment thereof containing at least one site for said post-translational modification;

(3) generating one or more capture agent(s) for each of said PETs identified in

(2), each of said capture agent(s) specifically bind one of said PETs for which said capture agent(s) is generated;

(4) fabricating arrays of capture agent(s) generated in (3) on solid support, wherein each of said capture agents is bound to a different discrete region of said solid support;

(5) packaging said arrays of capture agent(s) in (4) for diagnosis and/or research use in commercial and/or academic laboratories.

90. The business method of claim 89, further comprising marketing said arrays of capture agent(s) in (4) or said packaged arrays of capture agent(s) in (5) to potential customers and/or distributors.

91. The business method of claim 89, further comprising distributing said arrays of capture agent(s) in (4) or said packaged arrays of capture agent(s) in (5) to customers and/or distributors.

92. A business method for generating arrays of capture agents for marketing in research and development, the method comprising:

(1) identifying one or more protein(s), a post-translational modification of which protein(s) represent the activation of at least one signal transduction pathway within an organism;

(2) identifying one or more PETs for each of said protein(s), or fragment thereof containing at least one site for said post-translational modification;

(3) licensing to a third party the right to manufacture or use said one or more PET(s) identified in (2).

93. A method of immunizing a host animal against a disease condition associated with the presence or overexpression of a protein, comprising:

(1) computationally analyzing the amino acid sequence of said protein to identify one or more PET(s) unique to said protein within the proteome of said host animal;

(2) administering a peptide immunogen comprising said one or more PET(s) identified in (1) to said host animal.

94. The method of claim 93, wherein said one or more PET(s) is administered to said host animal in a formulation designed to enhance the immune response of said host animal.

95. The method of claim 94, wherein said formulation comprises liposomes with or without additional adjuvants selected from: lipopolysaccharide (LPS), lipid A, muramyl dipeptide (MDP), glucan or cytokine.

96. The method of claim 94, wherein said cytokine is an interleukin, an interferon, or an colony stimulating factor.

97. The method of claim 94, wherein said formulation comprises a viral or bacterial vector encoding said one or more PET(s).

98. The method of claim 93, wherein said protein is from an organism different from the host animal.

99. The method of claim 93, wherein said protein is from a tumor cell, an infectious agent or a parasitic agent.

100. The method of claim 93, wherein said infectious agent is SARS virus.

101. A method of generating antibodies specific for a marker protein for use in immunohistochemistry, the method comprising computationally analyzing the amino acid sequence of said marker protein to identify one or more PET(s) unique to said marker protein, wherein said PET(s) is located on the surface of said marker protein.

102. The method of claim 101, wherein said PET(s) excludes residues known to form cross-links under the fixation condition to be used in immunohistochemistry.

103. A method for simultaneous unambiguous detection / quantification of a family of related proteins in a sample, comprising:

(1) computationally analyzing amino acid sequences for said family of related proteins expected to be present in a sample of proteins, and identifying a common PET sequence unique to the said family of proteins;

(2) generating a capture agent that selectively and specifically binds said common PET;

(3) contacting said sample with said capture agent identified in (2); and

(4) detecting the presence and/or measuring the amount of proteins bound to said capture agent, thereby simultaneously detecting / quantifying said family of related proteins in said sample.

104. The method of claim 103, wherein said family of related proteins are denatured and digested by protease or chemical agents prior to step (3).

105. The method of claim 103, further comprising identifying at least one PET unique to each member of said family of related proteins to facilitate detection / quantification of said each member.

106. The method of claim 103, wherein said family of related proteins comprises a family of related kinases or cytokines.

107. The method of claim 103, wherein said sample is a body fluid selected from: saliva, mucous, sweat, whole blood, serum, urine, amniotic fluid, genital fluid, fecal material, marrow, plasma, spinal fluid, pericardial fluid, gastric fluid, abdominal fluid, peritoneal fluid, pleural fluid, synovial fluid, cyst fluid, cerebrospinal fluid, lung lavage fluid, lymphatic fluid, tears, prostatitc fluid, extraction from other body parts, or secretion from other glands; or from supernatant, whole cell lysate, or cell fraction obtained by lysis and fractionation of cellular material, extract or fraction of cells obtained directly from a biological entity or cells grown in an artificial environment.

108. A method of processing a sample for use in PET-associated detection / quantitation of a target protein therein, the method comprising denaturing all proteins of said sample, and/or fragmenting all proteins of said sample by a protease, a chemical agent, physical shearing, or sonication.

109. The method of claim 108, wherein said denaturation is thermo-denaturation or chemical denaturation.

110. The method of claim 109, wherein said thermo-denaturation is followed by or concurrent with proteolysis using thermo-stable proteases.

111. The method of claim 109, wherein said thermo-denaturation comprises two or more cycles of thermo-denaturation followed by protease digestion.

112. The method of claim 111, wherein each of said two or more cycles of thermo-denaturation is carried out by denaturing at about 90°C followed by protease digestion at about 50°C.

113. The method of claim 108, wherein said fragmentation is carried out by a protease selected from trypsin, chymotrypsin, pepsin, papain, carboxypeptidase, calpain, subtilisin, gluc-C, endo lys-C, or proteinase K.

114. The method of claim 108, wherein said sample is a body fluid selected from: saliva, mucous, sweat, whole blood, serum, urine, amniotic fluid, genital fluid, fecal material, marrow, plasma, spinal fluid, pericardial fluid, gastric fluid, abdominal fluid, peritoneal fluid, pleural fluid, synovial fluid, cyst fluid, cerebrospinal fluid, lung lavage fluid, lymphatic fluid, tears, prostatitc fluid, extraction from other body parts, or secretion from other glands; or from supernatant, whole cell lysate, or cell fraction obtained by lysis and fractionation of cellular material, extract or fraction of cells obtained directly from a biological entity or cells grown in an artificial environment.

115. The method of claim 108, wherein said target protein forms or tends to form complexes or aggregates with other proteins within said sample.

116. The method of claim 115, wherein said target protein is a TGF-beta protein.

117. A SARS virus-specific PET amino acid sequence as listed in Table SARS.

118. A method of generating antibodies specific for a PET sequence, the method comprising:

(1) administering to an animal a peptide immunogen comprising said PET sequence;

(2) screening for antibodies specific for said PET sequence using a peptide fragment comprising said PET sequence, said peptide fragment predictably results from a treatment of a protein comprising said PET sequence.

119. The method of claim 118, wherein said peptide immunogen consists essentially of said PET sequence.

120. The method of claim 118, wherein the N- or C-terminus, or both, of said PET sequence are blocked to eliminate free N- or C-terminus, or both.

121. The method of claim 118, wherein more than one peptide immunogens, each comprising a PET sequence, are administered to said animal.

122. The method of claim 121, wherein said more than one peptide immunogens encompasses PET sequences derived from different proteins.

123. The method of claim 118, wherein said peptide immunogen comprises more than one PET sequences.

124. The method of claim 123, wherein said more than one PET sequences are linked by short linker sequences.

125. The method of claim 123, wherein said more than one PET sequences are derived from different proteins.